

Summs	ary of cosmid clones	isolated from M. echi	Summary of cosmid clones isolated from M. echinospora genomic library.	
clone ^a	type I PKS genes ^b	type I PKS genes ^b type II PKS genes ^b deoxy sugar genes ^b	deoxy sugar genes ^b	resistance $(\mu \mathrm{g \ mL}^{-1})^{\mathcal{C}}$
3a	$N.D.^d$	N.D. ^d	N.D.ª	0.5
4a	N.D. ^d	N.D. ^d	N.D. ^d	6.5
4b	+	+	+	0.5
10a	+	+	+	0.5
13a	+	+	- 1 -	0.5
16a	$N.D.^d$	$N.D.^d$	N.D. ^d	0.5
56	+	+	+	0.1
58	1	: " 	+	< 0.01
09	.: +	+	+	0.05
99	ı	1	+	0.04
puc18/pBluescript ^e	1	Ĭ	1	< 0.01
		The second secon	The second secon	

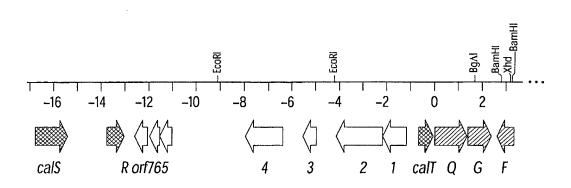
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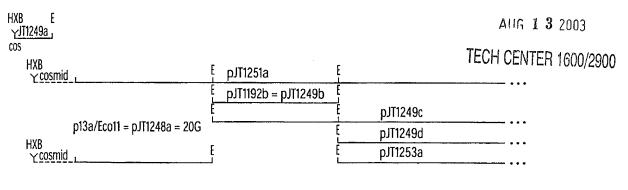
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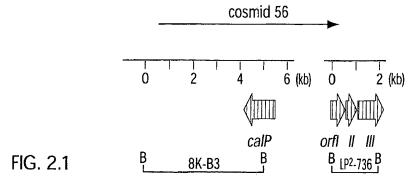




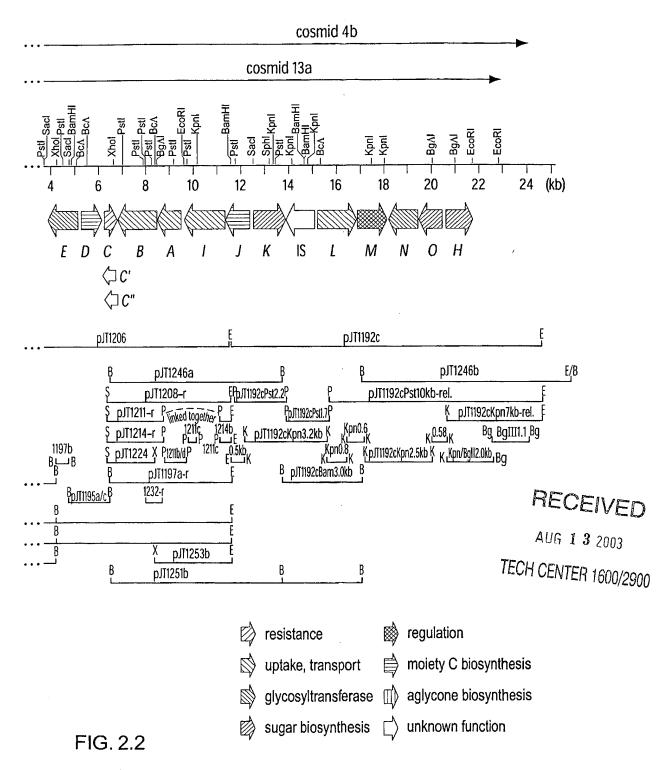
HXB Bg/Sau

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Putative number of polypeptide amino acids proposed fusction or sequence similarity detected simil		**					
CalB 56 membrane transporter calicheamicin resistance protein calicheamicin calicheamicin protein calicheamicin calicheam	1	pulative			probability		
CalC	Ì						DrrA ⁹⁷
CaID 263							рив,
CallE 420 glycosyltransferase 4.7x10 ³ -0 GTG/TAG EryCII ⁹⁹ CalF 245 M,N-dimethyltransferase 1.5x10 ⁻⁷⁸ ATG/TGA DesVI ¹⁰⁰ CalH 338 Perosamine synthetase confirmed GTG/TAG CalH 338 Perosamine synthetase confirmed GTG/TGA CalH 338 Perosamine synthetase confirmed GTG/TGA CalH 332 O-methyltransferase 1.0x10 ⁻⁷³ ATG/TGA DeiAE CalM 440 L-cysteine/cystine C-S-lyase 1.6x10 ⁻²⁸ GTG/TGA C-DES CalM 440 L-cysteine/cystine C-S-lyase 1.6x10 ⁻²⁸ GTG/TGA C-DES CalM 446 Calm 398 Glycosyltransferase 3.4x10 ⁻⁷⁹ ATG/TGA OppA GTG/TGA C-DES CalM 398 Glycosyltransferase 3.4x10 ⁻⁷⁹ ATG/TGA OppA CalO 331 Hexopyranosyl-2,3-reductase 4.9x10 ⁻¹³⁹ ATG/TGA C-tl GTG/TGA C-tl CalM 453 UDP-D-glucose 6-dehydrogenase confirmed CalR 282 Transcriptional regulator 6.7x10 ⁻¹¹ ATG/TGA ATG/TGA C-tl GTG/TGA CalF 213 Ps ₅₀ oxidase 2.9x10 ⁻⁶² GTG/TGA ATG/TGA SC5C7.03 GTG/TGA CalW 432 oxygenase/halogenase 2.0x10 ⁻⁶² GTG/TGA ATG/TGA SC5C7.03 GTG/TGA CalW 449 cytochrome P450 1.0x10 ⁻⁹¹ ATG/TGA ATG/TGA CYP105B1 CalW 449 cytochrome P450 1.0x10 ⁻⁹¹ ATG/TGA ATG/TGA CYP105B1 ActlI 136 polyketide cyclase 3.0x10 ⁻⁶⁴ ATG/TGA ATG/TGA Artiford ActlI 136 polyketide cyclase 3.0x10 ⁻⁶⁴ ATG/TGA ATG/TGA Artiford ActlI 136 polyketide cyclase 3.0x10 ⁻⁶⁴ ATG/TGA ATG/TGA Artiford ActlI 136 polyketide cyclase 3.0x10 ⁻⁶⁴ ATG/TGA ATG/TGA Artiford Artiford ActlI 136 polyketide cyclase 3.0x10 ⁻⁶⁴ ATG/TGA ATG/TGA Artiford ActlI 136 polyketide cyclase 3.0x10 ⁻⁶⁴ ATG/TGA ATG/TGA Artiford A	١						A 210 D X / 1198
CalF 245	1						
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CalH 338 Perosamine synthetase confirmed GTG/TGA DicALE CalI 568 Dipeptide transporter 1.7×10-24 GTG/TGA DicALE CalIK 440 L-cysteine/cystine C-S-lyase 1.6×10-28 GTG/TGA C-DES CalIK 562 Oligopeptide transporter protein 9.5×10-14 GTG/TGA C-DES CalM 416 Regulatory protein 9.5×10-14 ATG/TGA OppA CalN 398 Glycosyltransferase 3.4×10-79 ATG/TGA Ole1 CalO 331 Hexopyranosyl-2,3-reductase 4.9×10-139 ATG/TGA Ole1 CalQ 453 UDP-Dejlucose 6-dehydrogenase confirmed GTG/TGA Ctl CalR 282 Transcriptional regulator 6.7×10-11 ATG/TGA GTG/TGA CalT 432 oxygenase/halogenase 2.0×10-65 GTG/TGA SCSC7.03 CalT 432 oxygenase/halogenase 2.0×10-65 ATG/TGA ScG4/P CalW (449) cytochr	1						Desvi
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CalP							
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FIG. 3



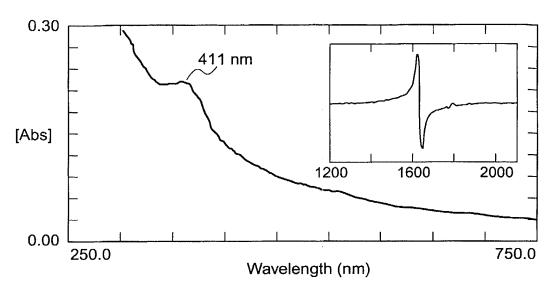


FIG. 4A

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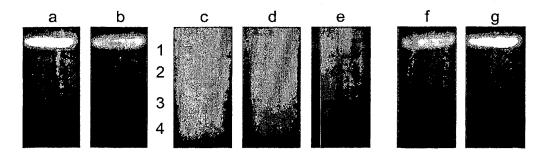
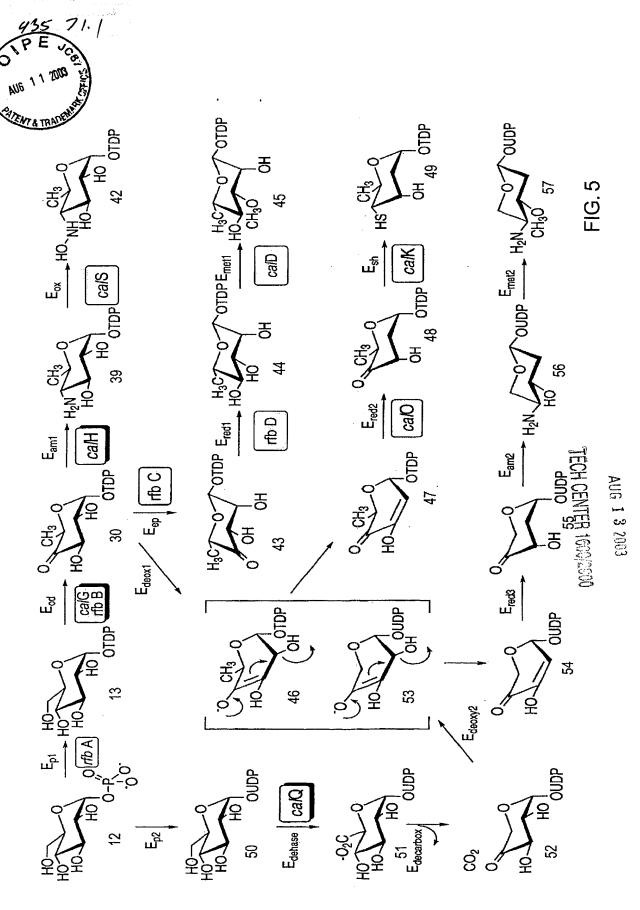
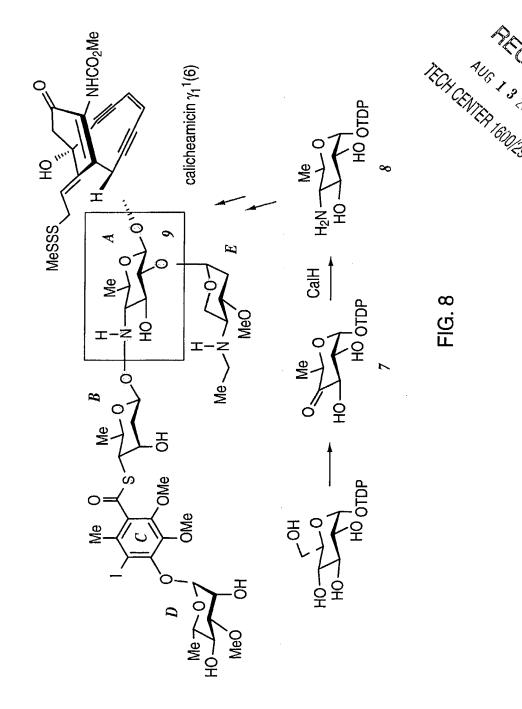
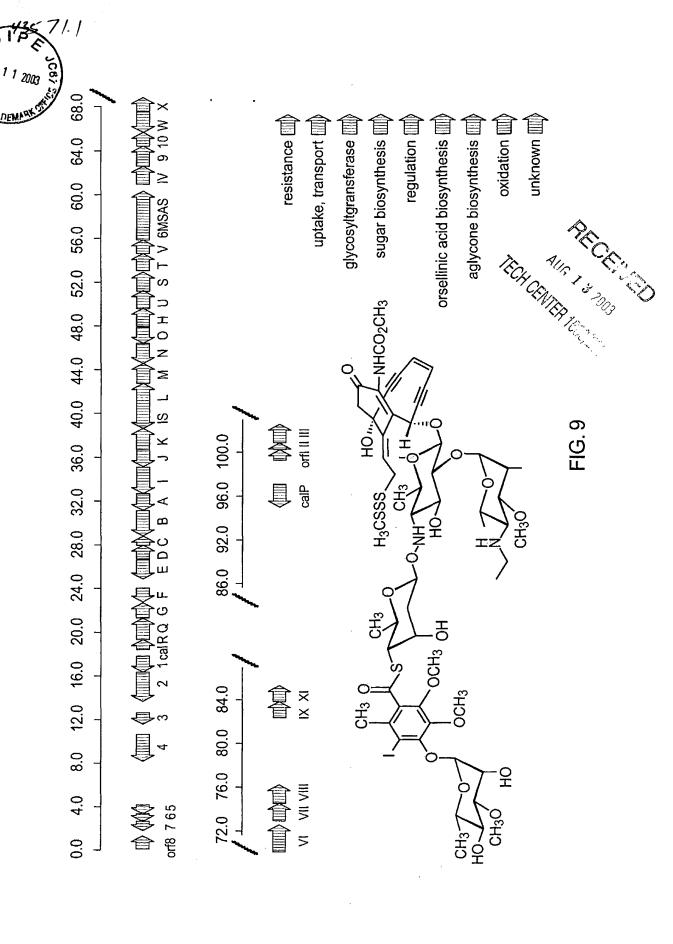
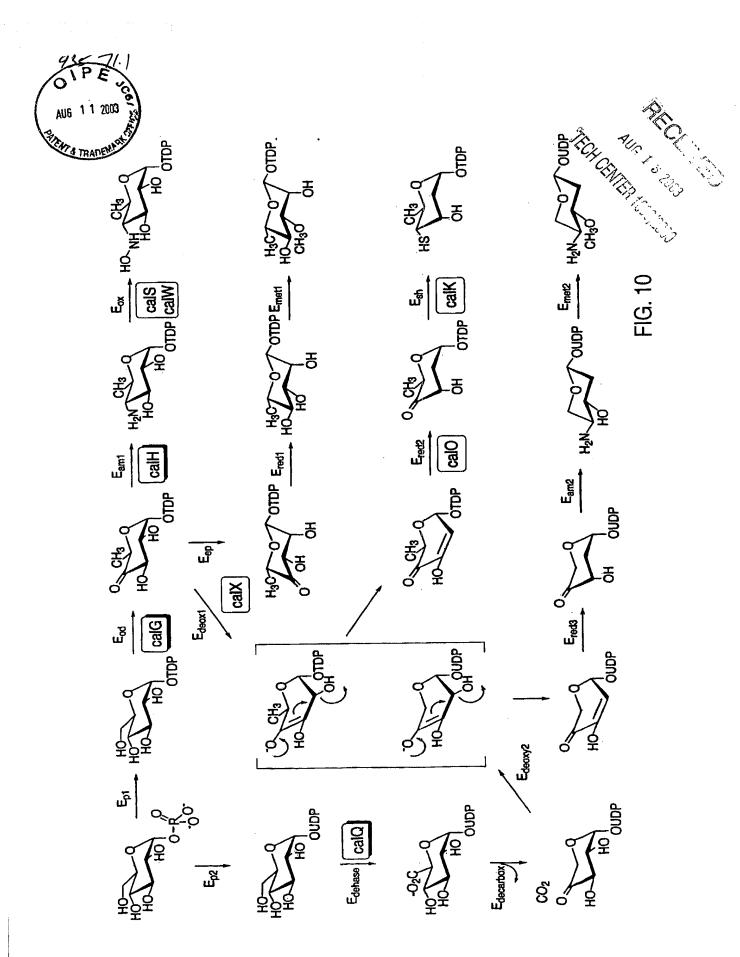


FIG. 4B











The Aryltetrasaccharide Unit (a type I PKS product):

"halogenase"

CalT

oxidation

calS calW

Call Call

Synthesis of Putative Substrates:

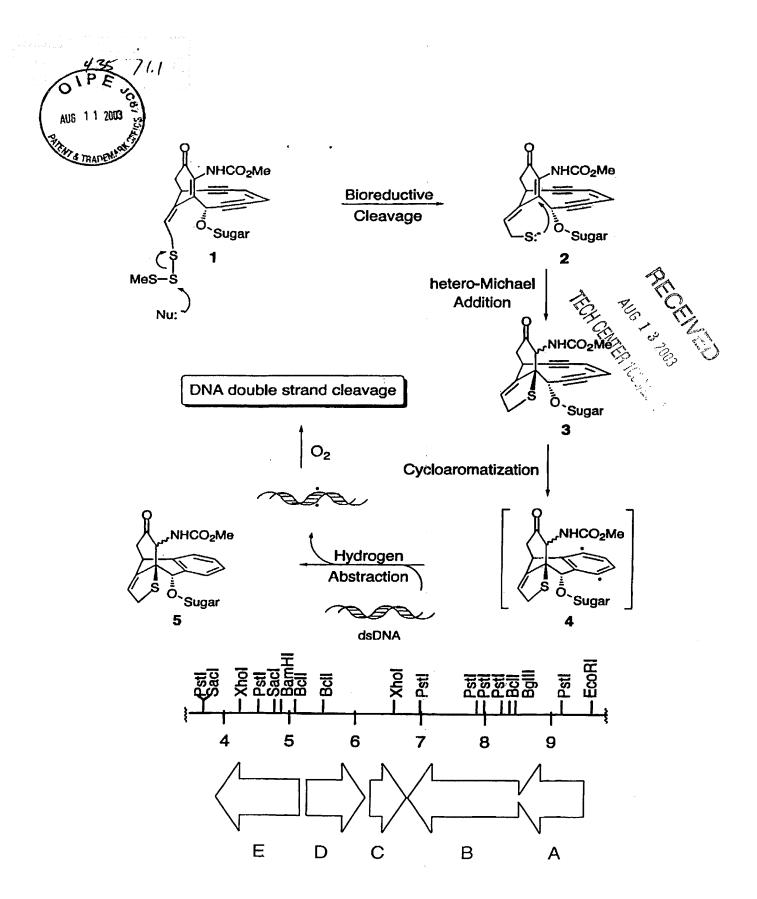
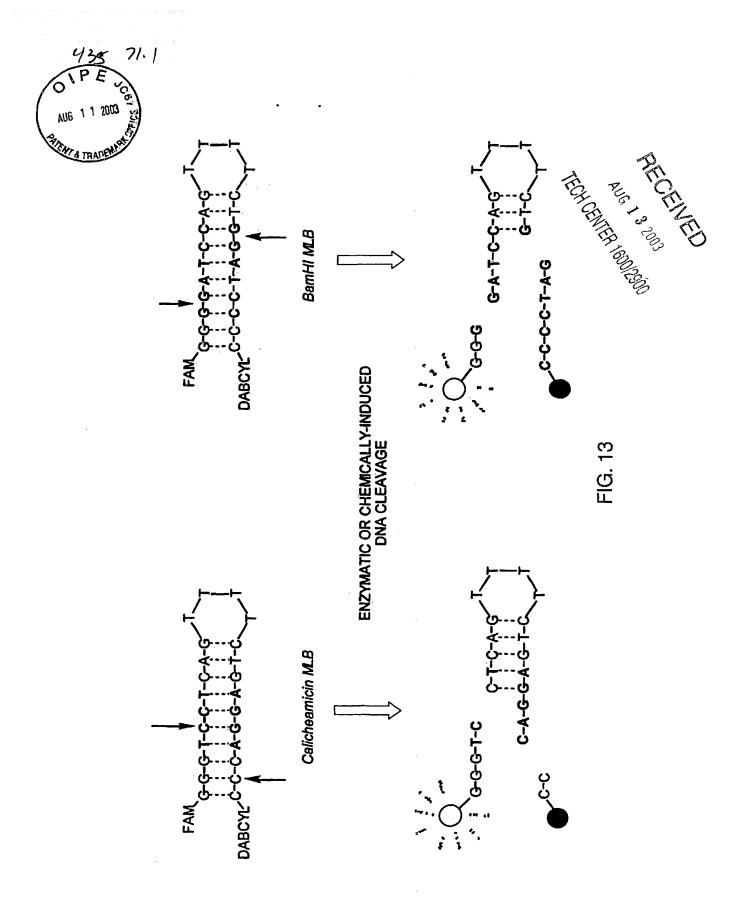
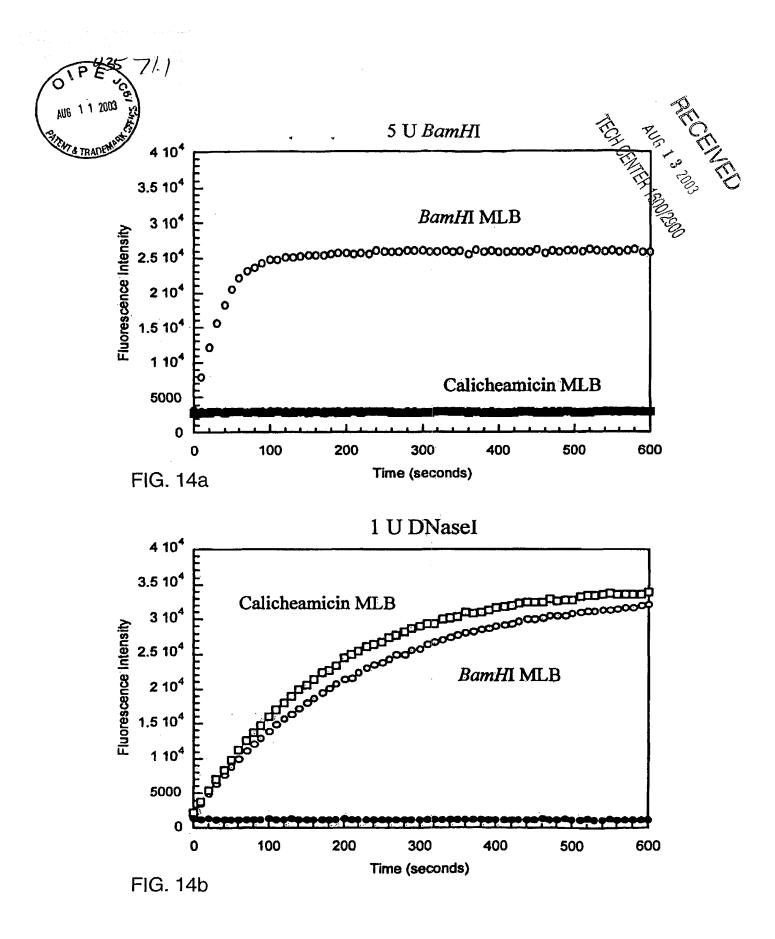


FIG. 12







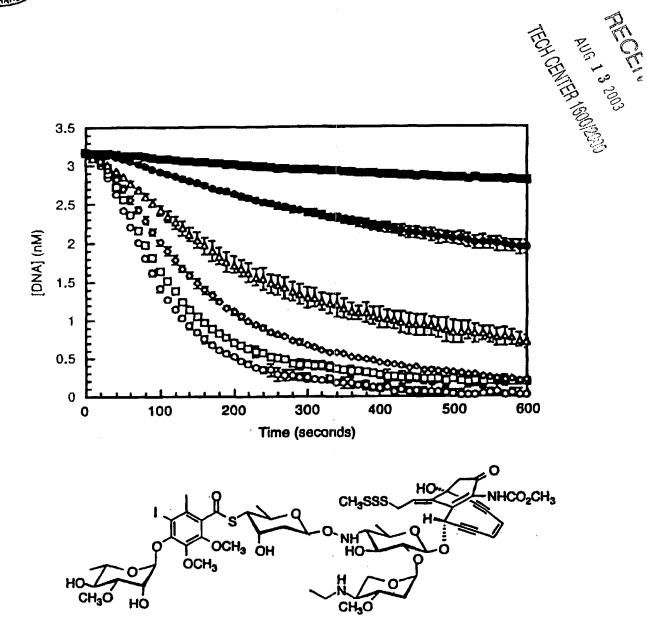


FIG. 15a



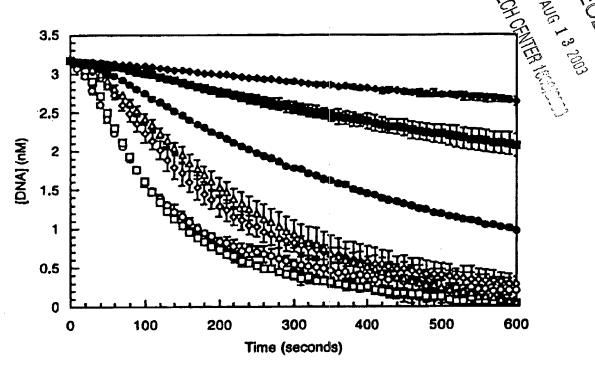
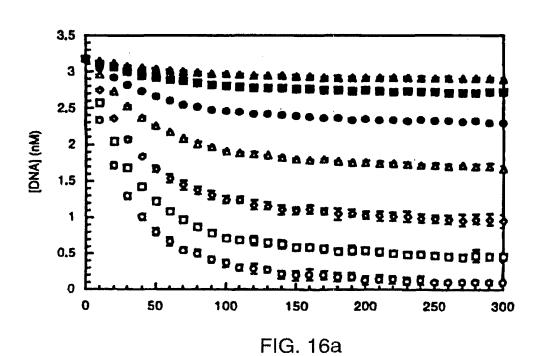


FIG. 15b



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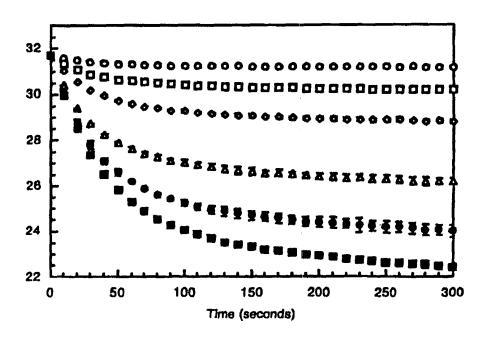
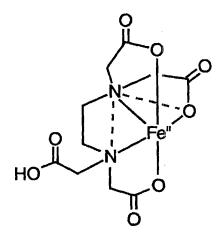


FIG.16c





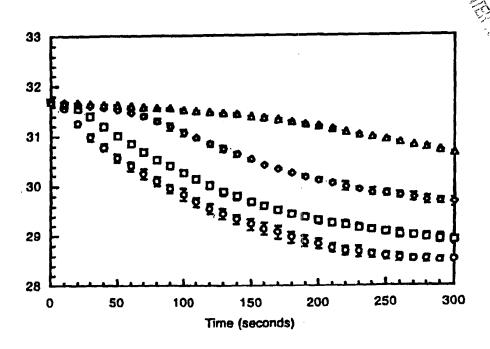


FIG. 16d

